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Alberghina, Lilia

<130> 3912.1000-000

<141> 2005-05-06

<151> 2003-11-06

<151> 2002-11-07

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<213> Saccharomyces cerevisiae

<220>

<221> sig peptide

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<213> Saccharomyces cerevisiae

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-15

-10

-5

Ala Leu Ala

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 gtgcaagaaa accaaaaagc aacaacaggt tttggataag tacatatata agagggcctt 180  
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 Ile Pro Ala Glu Ala Val Ile Gly Tyr Leu Asp Leu Glu Gly Asp Phe  
 -50 -45 -40  
 Asp Val Ala Val Leu Pro Phe Ser Asn Ser Thr Asn Asn Gly Leu Leu  
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 -20 -15 -10  
 Ser Leu Asp Lys Arg  
 -5

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<220>  
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 <222> (1)...(63)

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 <213> *Aspergillus niger*

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<222> (1)...(31)

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-15 -10 -5

<210> 9  
<211> 63  
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<213> Aspergillus oryzae

<220>  
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<222> (1)...(63)

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gcc 63

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 <213> Bacillus amyloliquefaciens

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 <222> (1)...(17)

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 Ala

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 <212> DNA  
 <213> *Saccharomycopsis fibuligera*

<220>  
 <221> sig\_peptide  
 <222> (1)...(51)

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 <212> PRT  
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<220>  
 <221> SIGNAL  
 <222> (1)...(17)

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<210> 17  
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 <212> DNA  
 <213> *Hypocrea pecorina*

<220>  
 <221> sig\_peptide  
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 <213> *Hypocrea pecorina*

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 <221> SIGNAL  
 <222> (1)...(22)

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 Ala Arg Leu Val Ala Ala  
           -5

<210> 19  
 <211> 63  
 <212> DNA  
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<220>  
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 <222> (1)...(63)

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<220>  
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 <222> (1)...(21)

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 Gly Gly Ala Val Ala  
           -5

<210> 21  
 <211> 48  
 <212> DNA  
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<220>  
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 <222> (1)...(48)

<400> 21  
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<210> 22  
 <211> 18  
 <212> PRT  
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<220>  
<221> SIGNAL  
<222> (1)...(18)

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Asp Ser

<210> 23  
<211> 57  
<212> DNA  
<213> Homo sapiens

<220>  
<221> sig\_peptide  
<222> (1)...(57)

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<213> Homo sapiens

<220>  
<221> SIGNAL  
<222> (1)...(19)

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<210> 25  
<211> 75  
<212> DNA  
<213> Rhizopus oryzae

<220>  
<221> sig\_peptide  
<222> (1)...(75)

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<210> 26  
<211> 25  
<212> PRT  
<213> Rhizopus oryzae

<220>  
<221> SIGNAL  
<222> (1)...(25)

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-25 -20 -15 -10  
Ser Tyr Phe Ser Leu Leu Val Ser Ala  
-5

<210> 27  
<211> 48  
<212> DNA  
<213> *Aspergillus niger*

<220>  
<221> sig\_peptide  
<222> (1)...(48)

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<210> 28  
<211> 16  
<212> PRT  
<213> *Aspergillus niger*

<220>  
<221> SIGNAL  
<222> (1)...(16)

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-15 -10 -5

<210> 29  
<211> 54  
<212> DNA  
<213> *Homo sapiens*

<220>  
<221> sig\_peptide  
<222> (1)...(54)

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<210> 30  
<211> 18  
<212> PRT  
<213> *Homo sapiens*

<220>  
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<222> (1)...(18)

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&lt;400&gt; 30

Met Lys Trp Val Thr Phe Ile Ser Leu Leu Phe Leu Phe Ser Ser Ala  
                   -15                  -10                  -5  
 Tyr Ser

&lt;210&gt; 31

&lt;211&gt; 78

&lt;212&gt; DNA

<213> *Saccharomyces cerevisiae*

&lt;220&gt;

&lt;221&gt; sig\_peptide

&lt;222&gt; (1)...(78)

&lt;400&gt; 31

atgacgaagc caacccaagt attagttaga tccgtcagta tattatTTTT catcacatta 60  
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&lt;210&gt; 32

&lt;211&gt; 26

&lt;212&gt; PRT

<213> *Saccharomyces cerevisiae*

&lt;220&gt;

&lt;221&gt; SIGNAL

&lt;222&gt; (1)...(26)

&lt;400&gt; 32

Met Thr Lys Pro Thr Gln Val Leu Val Arg Ser Val Ser Ile Leu Phe  
           -25                  -20                  -15  
 Phe Ile Thr Leu Leu His Leu Val Val Ala  
 -10                  -5

&lt;210&gt; 33

&lt;211&gt; 63

&lt;212&gt; DNA

<213> *Saccharomyces cerevisiae*

&lt;220&gt;

&lt;221&gt; sig\_peptide

&lt;222&gt; (1)...(63)

&lt;400&gt; 33

atgggccact tagcgatcct tttcagtatt atcgctgtat tgaatatagc tacagctgtt 60  
 gca 63

&lt;210&gt; 34

&lt;211&gt; 21

&lt;212&gt; PRT

<213> *Saccharomyces cerevisiae*

&lt;220&gt;

&lt;221&gt; SIGNAL

&lt;222&gt; (1)...(21)

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 Ala Thr Ala Val Ala  
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<210> 35  
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<220>  
 <221> sig\_peptide  
 <222> (1)...(48)

<400> 35  
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<210> 36  
 <211> 17  
 <212> PRT  
 <213> Kluyveromyces lactis

<220>  
 <221> SIGNAL  
 <222> (1)...(17)

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 Leu

<210> 37  
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 <213> Kluyveromyces lactis

<220>  
 <221> sig\_peptide  
 <222> (1)...(69)

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 atactcatc 69

<210> 38  
 <211> 23  
 <212> PRT  
 <213> Kluyveromyces lactis

<220>  
 <221> SIGNAL  
 <222> (1)...(23)

&lt;400&gt; 38

Met Lys Ile Tyr His Ile Phe Ser Val Cys Tyr Leu Ile Thr Leu Cys  
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Ala Ala Ala Ala Thr Thr Ala  
                  -5

&lt;210&gt; 39

&lt;211&gt; 54

&lt;212&gt; DNA

<213> *Saccharomyces cerevisiae*

&lt;220&gt;

&lt;221&gt; sig\_peptide

&lt;222&gt; (1)...(54)

&lt;400&gt; 39

atgtttgctt tctactttct caccgcatgc atcagtttga agggcgtttt tggg 54

&lt;210&gt; 40

&lt;211&gt; 18

&lt;212&gt; PRT

<213> *Saccharomyces cerevisiae*

&lt;220&gt;

&lt;221&gt; SIGNAL

&lt;222&gt; (1)...(18)

&lt;400&gt; 40

Met Phe Ala Phe Tyr Phe Leu Thr Ala Cys Ile Ser Leu Lys Gly Val  
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Phe Gly

&lt;210&gt; 41

&lt;211&gt; 54

&lt;212&gt; DNA

<213> *Saccharomyces cerevisiae*

&lt;220&gt;

&lt;221&gt; sig\_peptide

&lt;222&gt; (1)...(54)

&lt;400&gt; 41

atgtttaagt ctgttggtta ttcggttcta gccgctgctt tagttaatgc aggt 54

&lt;210&gt; 42

&lt;211&gt; 18

&lt;212&gt; PRT

<213> *Saccharomyces cerevisiae*

&lt;220&gt;

&lt;221&gt; SIGNAL

&lt;222&gt; (1)...(18)

&lt;400&gt; 42

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Met Phe Lys Ser Val Val Tyr Ser Val Leu Ala Ala Ala Leu Val Asn  
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Ala Gly

<210> 43  
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<220>  
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<222> (1)...(17)

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Ala

<210> 45  
<211> 48  
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<220>  
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<210> 46  
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<212> PRT  
<213> *Kluyveromyces lactis*

<220>  
<221> SIGNAL  
<222> (1)...(16)

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-15

-10

-5

&lt;210&gt; 47

&lt;211&gt; 48

&lt;212&gt; DNA

&lt;213&gt; Kluyveromyces lactis

&lt;220&gt;

&lt;221&gt; sig\_peptide

&lt;222&gt; (1)...(48)

&lt;400&gt; 47

atgctatcta ttctgttggg tttattatca ctatcaggga cccatgcg

48

&lt;210&gt; 48

&lt;211&gt; 16

&lt;212&gt; PRT

&lt;213&gt; Kluyveromyces lactis

&lt;220&gt;

&lt;221&gt; SIGNAL

&lt;222&gt; (1)...(16)

&lt;400&gt; 48

Met Leu Ser Ile Leu Leu Gly Leu Leu Ser Leu Ser Gly Thr His Ala

-15

-10

-5

&lt;210&gt; 49

&lt;211&gt; 54

&lt;212&gt; DNA

&lt;213&gt; Aspergillus niger

&lt;220&gt;

&lt;221&gt; sig\_peptide

&lt;222&gt; (1)...(54)

&lt;400&gt; 49

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54

&lt;210&gt; 50

&lt;211&gt; 18

&lt;212&gt; PRT

&lt;213&gt; Aspergillus niger

&lt;220&gt;

&lt;221&gt; SIGNAL

&lt;222&gt; (1)...(18)

&lt;400&gt; 50

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-15

-10

-5

Thr Ser

<210> 51  
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 <212> DNA  
 <213> *Saccharomyces cerevisiae*

<220>  
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 <222> (1)...(57)

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<220>  
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 <222> (1)...(19)

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 <222> (1)...(63)

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 <222> (1)...(21)

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 Asn Ser Ala Leu Gly  
 -5

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 <222> (1)...(21)

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 -5

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<220>  
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 <222> (1)...(96)

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 <211> 32  
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<220>  
 <221> SIGNAL  
 <222> (1)...(32)

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 -15 -10 -5

<210> 59  
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 <213> *Zygosaccharomyces bailii*

<220>  
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 <222> (1)...(63)

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 gct 63

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 <222> (1)...(21)

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 Ile Tyr Thr Ser Ala  
 -5

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 <212> DNA  
 <213> *Zygosaccharomyces bailii*

<220>  
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 <222> (1)...(417)

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 gaagaaattt ttacagattt gacgtatcac attcacgtta acgtcagtgg cgaaattgac 180  
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 agatatatat acgctatatt tacacagcag acaaactata cagaggatgg gctcattgag 300  
 tacttaaatc attacgattc agagacttgc aaagatatca ttactcagta taatgttaac 360  
 gtagacacta gtaactgtat aagcaatact acagatcaag ctagactcca acgtc 415

<210> 62  
 <211> 139  
 <212> PRT  
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<220>  
 <221> SIGNAL  
 <222> (1)...(139)

<400> 62

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Ile Tyr Thr Ser Ala Arg Asn Ile Leu Asp Arg Glu Tyr Thr Ala Asn
      -120                -115                -110
Glu Leu Lys Thr Ala Phe Gly Asp Glu Glu Ile Phe Thr Asp Leu Thr
      -105                -100                -95
Tyr His Ile His Val Asn Val Ser Gly Glu Ile Asp Ser Tyr Tyr His
      -90                -85                -80
Asn Leu Val Asn Phe Val Asp Asn Ala Leu Ala Asn Lys Asp Ile Asn
      -75                -70                -65
Arg Tyr Ile Tyr Ala Ile Phe Thr Gln Gln Thr Asn Tyr Thr Glu Asp
      -55                -50                -45
Gly Leu Ile Glu Tyr Leu Asn His Tyr Asp Ser Glu Thr Cys Lys Asp
      -40                -35                -30
Ile Ile Thr Gln Tyr Asn Val Asn Val Asp Thr Ser Asn Cys Ile Ser
      -25                -20                -15
Asn Thr Thr Asp Gln Ala Arg Leu Gln Arg Arg
      -10                -5

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&lt;210&gt; 63

&lt;211&gt; 587

&lt;212&gt; DNA

<213> *Zygosaccharomyces bailii*

&lt;400&gt; 63

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taactcaagg gggagtagtt ttgaggatca catgggaagt atttaaataa atagtagttc 180
ttttgtttta aaaaggcctc tccaaaagta atacttttag ggtaattact aagtataata 240
tatattataa gtaatagcct ttatagctta atggtaaagc agtaaaattga agatttacct 300
atatgtagtt cgattctcat taagggaagt ataaataagc tttttaatgg gccaatagct 360
gaaataagta atattattgt aaatattgag acttgaactc aaatcttatg cacctaaaaa 420
catatatttt aaccaattaa attatattta ctttattatt tacttatata acttctacta 480
attgtaaagt ataaccagct tttttgttaa caacaaaaac cgagaggggt catgttatat 540
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&lt;210&gt; 64

&lt;211&gt; 435

&lt;212&gt; DNA

<213> *Zygosaccharomyces bailii*

&lt;400&gt; 64

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ttaatttaat ttgtcgctaa ataataatgt tttaaataatt ataaatattt caaccaacca 60
cccccccaa aagggggtgg ttggtggttg gtcgtcacca accacctttg gtgggtggtg 120
ccccctatga gttttcatat tataaatata aaaactttta tggagggacc tataagaaat 180
aattgaggaa taattaataa taagttgcc tccttttttt tctcttctcc ccaccctaaa 240
aatactcctg ggggggggag ggagagaagt tatgtagtgg ggaggggtga agttaataat 300
agacttaaat agagttatat aaaataacat aaatatgctt aaaaataata ataataatat 360
taacagatag aagccaaagg gtcaggcgct ttctttggga gaaagagtta gttagttcga 420
atctatccta tctga 435

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&lt;210&gt; 65

&lt;211&gt; 299

&lt;212&gt; DNA

<213> *Zygosaccharomyces bailii*

<400> 65  
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 gagcttgacg gggaaagccg gcgaacgtgg cgagaaagga agggaagaaa gcgaaaggag 120  
 cgggcgctag ggcgctggca agtgtagcgg tcacgctgcg cgtaaccacc acaccgccc 180  
 cgcttaatgc gccgctacag ggcgctcag gtggcacttt tcggggaaat gtgcgcggaa 240  
 cccctatttg tttatttttc taaatacatt caaatatgta tccgctcatg agacaataa 299

<210> 66  
 <211> 153  
 <212> DNA  
 <213> *Zygosaccharomyces bailii*

<400> 66  
 ctccactgta acatttccca ctgtcctttt cccatctttc attttacaat gagcaagttt 60  
 cagaaaaaaa aatacaaatg ggataagtgc aaaacattcc atgtatctgt agcttccaat 120  
 gttattcctc tctccagagt caggcttctg tgt 153

<210> 67  
 <211> 231  
 <212> DNA  
 <213> *Zygosaccharomyces bailii*

<400> 67  
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 tctggagatt ttgcataaac aactgattta ttattagctt tattttctaa tccattaact 120  
 aattgatcat acataatata gatgaataag aataatgaaa ctagtgcaat aattgatcca 180  
 attgatgcta cataatttca accagcaaag gcatcagggt agtcaggaat t 231

<210> 68  
 <211> 52  
 <212> DNA  
 <213> *Zygosaccharomyces bailii*

<400> 68  
 ctcgtaaaaa cgagcatgag ctgcgtcagg tcagccgtgg atatcgttgc gg 52

<210> 69  
 <211> 116  
 <212> DNA  
 <213> *Zygosaccharomyces bailii*

<400> 69  
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 gctgctgcag gtgccgcagc cgaggcagcg cattttcgaa ctctacgccc agcgcg 116

<210> 70  
 <211> 268  
 <212> DNA  
 <213> *Zygosaccharomyces bailii*

<400> 70  
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 cctgggcata attgagcaaa tcgtactcgt gcgcggcgat gcgctccttg ccgatcgaat 120  
 tgacgtaatc gatcgcgcg cgcagcccga tcgcctcgac gatcggcggc gtgccggcct 180  
 cgaacttggt cggcggggtc ccataggtga cccagtcctt ggcaacttca cggatcattt 240  
 cgccgcggcc gttgaacggc cgcatcgc 268

<210> 71  
 <211> 869  
 <212> DNA  
 <213> *Zygosaccharomyces bailii*

<400> 71  
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 tcggtaccac gcatgctgca gacgcgttac gtatcggatc cagaattcgt gatattctat 120  
 tgggtatgtc ccctgattcg acggcgtaaa ttgcgtgaat ctgtgtgtgg cgctaattgac 180  
 cgctttttgg aattatgtgc tatgcctctg ccattgggat caacagctga aatattttgtt 240  
 gaagatcgaa tatcttctat tgtttctgag ggtatccccg aagctatggc gaaagaaagg 300  
 atctcttctc gtacttggat cggtagcaga agcaatagac gcacaatgca ttgacgcatac 360  
 ttgttgatac cgggtaaatgt gagtcttctg ggttctgtta ttgagtttaa tatgtcgtcc 420  
 acctctgttc tcgtatccat tttgcgagta gcccgccata cagcacgtcc aatacaggag 480  
 aggccattta gcttcagggtg cagagaagac acagcatggt gctcaccttc gagtgcctca 540  
 atagatgatt gagttgactg ggcttccgtg aaagggcctt tcgagagatc ttcagaaata 600  
 aaccagggtt gcgcttcatt agtaggtgtt cctggaggac tattgtcgct atctgctgga 660  
 ctactgctac caagtagtga aggggtatt ctaaggcttt cactctgttc tgacactatt 720  
 ataacattgc caaggccaat ttgaaagggt tcgcgtatat gagtaaagag ctcggtgccc 780  
 ttccagttgg aatcaagccg ttcaagcaga tcgagagcat aatcagagtc cacatttccg 840  
 cacgcaagag agaactctga gttcattct 869

<210> 72  
 <211> 1425  
 <212> DNA  
 <213> *Zygosaccharomyces bailii*

<220>  
 <221> CDS  
 <222> (1)...(1425)

<400> 72  
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 1 5 10 15  
 gca gaa ata aag cgt att ttg agt cgc ggc gac cct ata cct tta caa 96  
 Ala Glu Ile Lys Arg Ile Leu Ser Arg Gly Asp Pro Ile Pro Leu Gln  
 20 25 30  
 agg tta gct tct cta cta act atg gtg atc cta acg gtc aac atg tca 144  
 Arg Leu Ala Ser Leu Leu Thr Met Val Ile Leu Thr Val Asn Met Ser  
 35 40 45  
 aaa aag agg aag agc tct cca atc aag ctt agc acc ttt act aaa tat 192  
 Lys Lys Arg Lys Ser Ser Pro Ile Lys Leu Ser Thr Phe Thr Lys Tyr  
 50 55 60  
 cgt aga aat gtt gcg aag tca ttg tat tat gat atg tca agc aag aca 240  
 Arg Arg Asn Val Ala Lys Ser Leu Tyr Tyr Asp Met Ser Ser Lys Thr  
 65 70 75 80  
 gta ttc ttc gaa tac cat ctc aaa aat aca caa gat cta cag gag ggc 288  
 Val Phe Phe Glu Tyr His Leu Lys Asn Thr Gln Asp Leu Gln Glu Gly  
 85 90 95  
 ctc gag caa gcc att gcg ccc tac aat ttc gtg gta aag gtg cac aag 336

Leu	Glu	Gln	Ala	Ile	Ala	Pro	Tyr	Asn	Phe	Val	Val	Lys	Val	His	Lys	
			100					105					110			
aag	cca	att	gat	tgg	cag	aaa	cag	ctc	tca	agc	gtg	cat	gag	agg	aaa	384
Lys	Pro	Ile	Asp	Trp	Gln	Lys	Gln	Leu	Ser	Ser	Val	His	Glu	Arg	Lys	
		115					120					125				
gcg	ggc	cac	aga	agc	att	ctc	agc	aac	aat	gtt	ggc	gcc	gag	atc	tct	432
Ala	Gly	His	Arg	Ser	Ile	Leu	Ser	Asn	Asn	Val	Gly	Ala	Glu	Ile	Ser	
	130					135					140					
aaa	ctg	gct	gag	acg	aaa	gat	tct	act	tgg	agt	ttt	atc	gag	aga	aca	480
Lys	Leu	Ala	Glu	Thr	Lys	Asp	Ser	Thr	Trp	Ser	Phe	Ile	Glu	Arg	Thr	
145					150					155					160	
atg	gat	ctg	ata	gaa	gcc	cgc	acc	cgc	cag	ccc	acg	aca	aga	gtt	gcg	528
Met	Asp	Leu	Ile	Glu	Ala	Arg	Thr	Arg	Gln	Pro	Thr	Thr	Arg	Val	Ala	
				165					170					175		
tat	agg	ttt	ctg	ctt	caa	ctc	aca	ttc	atg	aac	tgc	tgt	agg	gct	aat	576
Tyr	Arg	Phe	Leu	Leu	Gln	Leu	Thr	Phe	Met	Asn	Cys	Cys	Arg	Ala	Asn	
			180					185					190			
gat	ttg	aaa	aac	gcc	gac	ccc	agc	act	ttt	caa	atc	atc	gca	gat	cct	624
Asp	Leu	Lys	Asn	Ala	Asp	Pro	Ser	Thr	Phe	Gln	Ile	Ile	Ala	Asp	Pro	
		195					200					205				
cac	ctt	ggt	cgt	ata	ttg	cgg	gcc	ttt	gtt	cca	gag	aca	aag	act	agc	672
His	Leu	Gly	Arg	Ile	Leu	Arg	Ala	Phe	Val	Pro	Glu	Thr	Lys	Thr	Ser	
	210					215					220					
att	gaa	agg	ttt	atc	tat	ttt	ttc	cca	tgt	aag	gga	cga	tgc	gat	ccg	720
Ile	Glu	Arg	Phe	Ile	Tyr	Phe	Phe	Pro	Cys	Lys	Gly	Arg	Cys	Asp	Pro	
225					230					235					240	
ctt	ttg	gct	cta	gat	tcc	tat	ctc	ctg	tgg	gtt	ggc	cca	gtg	ccc	aaa	768
Leu	Leu	Ala	Leu	Asp	Ser	Tyr	Leu	Leu	Trp	Val	Gly	Pro	Val	Pro	Lys	
				245					250					255		
act	cag	act	acc	gat	gaa	gag	act	caa	tat	gat	tac	cag	ctt	ctt	caa	816
Thr	Gln	Thr	Thr	Asp	Glu	Glu	Thr	Gln	Tyr	Asp	Tyr	Gln	Leu	Leu	Gln	
			260					265					270			
gat	act	ctc	ttg	att	tcg	tac	gac	agg	ttt	atc	gcc	aaa	gaa	tca	aag	864
Asp	Thr	Leu	Leu	Ile	Ser	Tyr	Asp	Arg	Phe	Ile	Ala	Lys	Glu	Ser	Lys	
		275					280					285				
gaa	aat	att	ttc	aaa	ata	cct	aat	ggg	ccc	aaa	gct	cat	ttg	ggg	cgg	912
Glu	Asn	Ile	Phe	Lys	Ile	Pro	Asn	Gly	Pro	Lys	Ala	His	Leu	Gly	Arg	
	290					295					300					
cat	cta	atg	gca	tca	tac	ctt	gga	aac	aac	agt	ctc	aag	agc	gag	gcc	960
His	Leu	Met	Ala	Ser	Tyr	Leu	Gly	Asn	Asn	Ser	Leu	Lys	Ser	Glu	Ala	
305					310					315					320	
aca	ctc	tac	ggc	aac	tgg	tct	gtg	gaa	agg	caa	gag	ggc	gtc	agc	aaa	1008
Thr	Leu	Tyr	Gly	Asn	Trp	Ser	Val	Glu	Arg	Gln	Glu	Gly	Val	Ser	Lys	

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325										330					335					
atg	gct	gac	agc	cga	tac	atg	cac	acg	ggt	aaa	aaa	agt	cca	cct	tca	1056				
Met	Ala	Asp	Ser	Arg	Tyr	Met	His	Thr	Val	Lys	Lys	Ser	Pro	Pro	Ser					
			340					345					350							
tat	cta	ttt	gca	ttt	tta	tcc	ggc	tac	tac	aaa	aag	tcc	aac	caa	ggc	1104				
Tyr	Leu	Phe	Ala	Phe	Leu	Ser	Gly	Tyr	Tyr	Lys	Lys	Ser	Asn	Gln	Gly					
		355					360					365								
gag	tac	gtg	ctg	gct	gaa	aca	ctg	tat	aat	ccc	ctg	gat	tac	gac	aaa	1152				
Glu	Tyr	Val	Leu	Ala	Glu	Thr	Leu	Tyr	Asn	Pro	Leu	Asp	Tyr	Asp	Lys					
		370				375					380									
aca	ctt	cca	ata	aca	acg	aac	gag	aaa	ttg	atc	tgt	cgg	cgg	tac	ggg	1200				
Thr	Leu	Pro	Ile	Thr		Asn	Glu	Lys	Leu	Ile	Cys	Arg	Arg	Tyr	Gly					
385					390				395						400					
aaa	aat	gcg	aaa	gtg	ata	cca	aaa	gac	gca	ctg	ctg	tat	ctc	tac	acg	1248				
Lys	Asn	Ala	Lys	Val	Ile	Pro	Lys	Asp	Ala	Leu	Leu	Tyr	Leu	Tyr	Thr					
			405					410						415						
tat	gcg	cag	cag	aag	cga	aaa	caa	ttg	gcc	gat	ccc	aat	gag	caa	aat	1296				
Tyr	Ala	Gln	Gln	Lys	Arg	Lys	Gln	Leu	Ala	Asp	Pro	Asn	Glu	Gln	Asn					
			420				425						430							
agg	cta	ttc	agt	agt	gaa	tca	cca	gcg	cat	ccc	ttc	tta	act	cct	caa	1344				
Arg	Leu	Phe	Ser	Ser	Glu	Ser	Pro	Ala	His	Pro	Phe	Leu	Thr	Pro	Gln					
		435				440					445									
tcg	aca	ggc	tca	tcg	aca	ccc	ttg	acc	tgg	act	gct	cca	aag	aca	ctc	1392				
Ser	Thr	Gly	Ser	Ser	Thr		Leu	Thr	Trp	Thr		Ala	Pro	Lys	Thr					
		450				455				460										
tcc	act	ggt	cta	atg	aca	cct	gga	gaa	gag	tag						1425				
Ser	Thr	Gly	Leu	Met	Thr	Pro	Gly	Glu	Glu	*										
465					470															

&lt;210&gt; 73

&lt;211&gt; 474

&lt;212&gt; PRT

&lt;213&gt; Zygosaccharomyces bailii

&lt;400&gt; 73

Met	Ser	Glu	Phe	Ser	Glu	Leu	Val	Arg	Ile	Leu	Pro	Leu	Asp	Gln	Val
1				5					10					15	
Ala	Glu	Ile	Lys	Arg	Ile	Leu	Ser	Arg	Gly	Asp	Pro	Ile	Pro	Leu	Gln
			20					25					30		
Arg	Leu	Ala	Ser	Leu	Leu	Thr	Met	Val	Ile	Leu	Thr	Val	Asn	Met	Ser
		35				40						45			
Lys	Lys	Arg	Lys	Ser	Ser	Pro	Ile	Lys	Leu	Ser	Thr	Phe	Thr	Lys	Tyr
		50				55					60				
Arg	Arg	Asn	Val	Ala	Lys	Ser	Leu	Tyr	Tyr	Asp	Met	Ser	Ser	Lys	Thr
65					70					75				80	
Val	Phe	Phe	Glu	Tyr	His	Leu	Lys	Asn	Thr	Gln	Asp	Leu	Gln	Glu	Gly
				85					90					95	

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Leu Glu Gln Ala Ile Ala Pro Tyr Asn Phe Val Val Lys Val His Lys
      100      105      110
Lys Pro Ile Asp Trp Gln Lys Gln Leu Ser Ser Val His Glu Arg Lys
      115      120      125
Ala Gly His Arg Ser Ile Leu Ser Asn Asn Val Gly Ala Glu Ile Ser
      130      135      140
Lys Leu Ala Glu Thr Lys Asp Ser Thr Trp Ser Phe Ile Glu Arg Thr
145      150      155      160
Met Asp Leu Ile Glu Ala Arg Thr Arg Gln Pro Thr Thr Arg Val Ala
      165      170      175
Tyr Arg Phe Leu Leu Gln Leu Thr Phe Met Asn Cys Cys Arg Ala Asn
      180      185      190
Asp Leu Lys Asn Ala Asp Pro Ser Thr Phe Gln Ile Ile Ala Asp Pro
195      200      205
His Leu Gly Arg Ile Leu Arg Ala Phe Val Pro Glu Thr Lys Thr Ser
210      215      220
Ile Glu Arg Phe Ile Tyr Phe Phe Pro Cys Lys Gly Arg Cys Asp Pro
225      230      235      240
Leu Leu Ala Leu Asp Ser Tyr Leu Leu Trp Val Gly Pro Val Pro Lys
      245      250      255
Thr Gln Thr Thr Asp Glu Glu Thr Gln Tyr Asp Tyr Gln Leu Leu Gln
      260      265      270
Asp Thr Leu Leu Ile Ser Tyr Asp Arg Phe Ile Ala Lys Glu Ser Lys
275      280      285
Glu Asn Ile Phe Lys Ile Pro Asn Gly Pro Lys Ala His Leu Gly Arg
290      295      300
His Leu Met Ala Ser Tyr Leu Gly Asn Asn Ser Leu Lys Ser Glu Ala
305      310      315      320
Thr Leu Tyr Gly Asn Trp Ser Val Glu Arg Gln Glu Gly Val Ser Lys
      325      330      335
Met Ala Asp Ser Arg Tyr Met His Thr Val Lys Lys Ser Pro Pro Ser
340      345      350
Tyr Leu Phe Ala Phe Leu Ser Gly Tyr Tyr Lys Lys Ser Asn Gln Gly
355      360      365
Glu Tyr Val Leu Ala Glu Thr Leu Tyr Asn Pro Leu Asp Tyr Asp Lys
370      375      380
Thr Leu Pro Ile Thr Thr Asn Glu Lys Leu Ile Cys Arg Arg Tyr Gly
385      390      395      400
Lys Asn Ala Lys Val Ile Pro Lys Asp Ala Leu Leu Tyr Leu Tyr Thr
      405      410      415
Tyr Ala Gln Gln Lys Arg Lys Gln Leu Ala Asp Pro Asn Glu Gln Asn
420      425      430
Arg Leu Phe Ser Ser Glu Ser Pro Ala His Pro Phe Leu Thr Pro Gln
435      440      445
Ser Thr Gly Ser Ser Thr Pro Leu Thr Trp Thr Ala Pro Lys Thr Leu
450      455      460
Ser Thr Gly Leu Met Thr Pro Gly Glu Glu
465      470

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&lt;210&gt; 74

&lt;211&gt; 1075

&lt;212&gt; DNA

&lt;213&gt; Zygosaccharomyces bailii

&lt;220&gt;

&lt;221&gt; CDS

&lt;222&gt; (1)...(1074)

&lt;400&gt; 74

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Met Phe Ser Arg Glu Glu Val Arg Ala Ser Arg Pro Thr Lys Glu Met	
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aag atg atc ttt gat gtg ctt atg aca ttt cct tac ttc gcg gta cat	96
Lys Met Ile Phe Asp Val Leu Met Thr Phe Pro Tyr Phe Ala Val His	
20 25 30	
gtt cct tcc aag aat ata ctt atc aca cca aaa ggc aca gtt gag ata	144
Val Pro Ser Lys Asn Ile Leu Ile Thr Pro Lys Gly Thr Val Glu Ile	
35 40 45	
cct gaa aac tat caa aat tat ccc ata ttg gcc atc ttc tac gtc aaa	192
Pro Glu Asn Tyr Gln Asn Tyr Pro Ile Leu Ala Ile Phe Tyr Val Lys	
50 55 60	
tat tta atg aag aaa aat ccg tac gat ctt ctt cca agc acc gtg aac	240
Tyr Leu Met Lys Lys Asn Pro Tyr Asp Leu Leu Pro Ser Thr Val Asn	
65 70 75 80	
tgg ccg gaa ccc tat gta gtg gtg aat acc atc act aag cgt ttc cag	288
Trp Pro Glu Pro Tyr Val Val Val Asn Thr Ile Thr Lys Arg Phe Gln	
85 90 95	
gac cat aaa cta ttt gca aac aaa aat gct gat gtc tac gtt gaa aga	336
Asp His Lys Leu Phe Ala Asn Lys Asn Ala Asp Val Tyr Val Glu Arg	
100 105 110	
ctt caa aat gca att gcc tcg ggt att aag att cct gag tct aag aag	384
Leu Gln Asn Ala Ile Ala Ser Gly Ile Lys Ile Pro Glu Ser Lys Lys	
115 120 125	
aat gaa cga tta ggg cag cca aaa aag acg aaa aat gtt aca aaa gag	432
Asn Glu Arg Leu Gly Gln Pro Lys Lys Thr Lys Asn Val Thr Lys Glu	
130 135 140	
aat tga gga gac ctt tat tga tgc cac taa tgc gag aaa aga att gga	480
Asn * Gly Asp Leu Tyr * Cys His * Cys Glu Lys Arg Ile Gly	
145 150 155	
tga gta ctt cag aaa act tca gga tgg tac att aac cgg aga ttt gga	528
* Val Leu Gln Lys Thr Ser Gly Trp Tyr Ile Asn Arg Arg Phe Gly	
160 165 170	
ggg tgg ctt gtg caa ggt caa aac gct cat atc gtg taa agc ttt gtt	576
Gly Trp Leu Val Gln Gly Gln Asn Ala His Ile Val * Ser Phe Val	
175 180 185	
cgg agg aca cac cca aga act cca gtt tat ggc cac caa tgt tcg taa	624
Arg Arg Thr His Pro Arg Thr Pro Val Tyr Gly His Gln Cys Ser *	
190 195 200	
agt ctg gat agg gga gat agt gtg cgg cat ggt ttc caa taa aaa tgc	672
Ser Leu Asp Arg Gly Asp Ser Val Arg His Gly Phe Gln * Lys Cys	

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205	210	215	
aat tga cga taa tga tct cga gga aga aga gcg taa tgc atc ggg cga			720
Asn * Arg * * Ser Arg Gly Arg Arg Ala * Cys Ile Gly Arg			
	220	225	
aca aac tac gac agc ccg aga gga atc aga ggc tct gga tac cac atc			768
Thr Asn Tyr Asp Ser Pro Arg Gly Ile Arg Gly Ser Gly Tyr His Ile			
	230	240	245
caa tgg ttt gga cgc tct gaa tac tca aat taa tgc cat aga aac gga			816
Gln Trp Phe Gly Arg Ser Glu Tyr Ser Asn * Cys His Arg Asn Gly			
	250	255	260
gga atc att ttg gga agc tat cag ggc gct cca taa tga gct acg cac			864
Gly Ile Ile Leu Gly Ser Tyr Gln Gly Ala Pro * * Ala Thr His			
	265	270	
ctc tcc aac aca gtt aga aga gtg cag gaa agc ggc agt ttt ttt act			912
Leu Ser Asn Thr Val Arg Arg Val Gln Glu Ser Gly Ser Phe Phe Thr			
	275	280	285
ggg cca taa aaa aat act cca aac att tac aaa gca aaa gga tac tgc			960
Gly Pro * Lys Asn Thr Pro Asn Ile Tyr Lys Ala Lys Gly Tyr Cys			
	295	300	305
ccg cgc tct ttt tta tat aaa tct caa aga gtg tct ggg aac cag ctg			1008
Pro Arg Ser Phe Leu Tyr Lys Ser Gln Arg Val Ser Gly Asn Gln Leu			
	310	315	320
gaa ttt aga ata tac aga ggc atc aga tgc aag aaa aat ggc aat taa			1056
Glu Phe Arg Ile Tyr Arg Gly Ile Arg Cys Lys Lys Asn Gly Asn *			
	325	330	335
agg tga gct tca aaa tta a			1075
Arg * Ala Ser Lys Leu			
	340		

&lt;210&gt; 75

&lt;211&gt; 341

&lt;212&gt; PRT

&lt;213&gt; Zygosaccharomyces bailii

&lt;400&gt; 75

Met Phe Ser Arg Glu Glu Val Arg Ala Ser Arg Pro Thr Lys Glu Met			
1 5 10 15			
Lys Met Ile Phe Asp Val Leu Met Thr Phe Pro Tyr Phe Ala Val His			
20 25 30			
Val Pro Ser Lys Asn Ile Leu Ile Thr Pro Lys Gly Thr Val Glu Ile			
35 40 45			
Pro Glu Asn Tyr Gln Asn Tyr Pro Ile Leu Ala Ile Phe Tyr Val Lys			
50 55 60			
Tyr Leu Met Lys Lys Asn Pro Tyr Asp Leu Leu Pro Ser Thr Val Asn			
65 70 75 80			
Trp Pro Glu Pro Tyr Val Val Val Asn Thr Ile Thr Lys Arg Phe Gln			
85 90 95			

Asp His Lys Leu Phe Ala Asn Lys Asn Ala Asp Val Tyr Val Glu Arg  
                   100                  105                  110  
 Leu Gln Asn Ala Ile Ala Ser Gly Ile Lys Ile Pro Glu Ser Lys Lys  
                   115                  120                  125  
 Asn Glu Arg Leu Gly Gln Pro Lys Lys Thr Lys Asn Val Thr Lys Glu  
                   130                  135                  140  
 Asn Gly Asp Leu Tyr Cys His Cys Glu Lys Arg Ile Gly Val Leu Gln  
                   145                  150                  155                  160  
 Lys Thr Ser Gly Trp Tyr Ile Asn Arg Arg Phe Gly Gly Trp Leu Val  
                   165                  170                  175  
 Gln Gly Gln Asn Ala His Ile Val Ser Phe Val Arg Arg Thr His Pro  
                   180                  185                  190  
 Arg Thr Pro Val Tyr Gly His Gln Cys Ser Ser Leu Asp Arg Gly Asp  
                   195                  200                  205  
 Ser Val Arg His Gly Phe Gln Lys Cys Asn Arg Ser Arg Gly Arg Arg  
                   210                  215                  220  
 Ala Cys Ile Gly Arg Thr Asn Tyr Asp Ser Pro Arg Gly Ile Arg Gly  
                   225                  230                  235                  240  
 Ser Gly Tyr His Ile Gln Trp Phe Gly Arg Ser Glu Tyr Ser Asn Cys  
                   245                  250                  255  
 His Arg Asn Gly Gly Ile Ile Leu Gly Ser Tyr Gln Gly Ala Pro Ala  
                   260                  265                  270  
 Thr His Leu Ser Asn Thr Val Arg Arg Val Gln Glu Ser Gly Ser Phe  
                   275                  280                  285  
 Phe Thr Gly Pro Lys Asn Thr Pro Asn Ile Tyr Lys Ala Lys Gly Tyr  
                   290                  295                  300  
 Cys Pro Arg Ser Phe Leu Tyr Lys Ser Gln Arg Val Ser Gly Asn Gln  
                   305                  310                  315                  320  
 Leu Glu Phe Arg Ile Tyr Arg Gly Ile Arg Cys Lys Lys Asn Gly Asn  
                   325                  330                  335  
 Arg Ala Ser Lys Leu  
                   340

&lt;210&gt; 76

&lt;211&gt; 750

&lt;212&gt; DNA

&lt;213&gt; Zygosaccharomyces bailii

&lt;220&gt;

&lt;221&gt; CDS

&lt;222&gt; (1)...(750)

&lt;400&gt; 76

atg aac tca gag ttc tct ctt gcg tac gga aat gtg gac tct gat tat 48  
 Met Asn Ser Glu Phe Ser Leu Ala Tyr Gly Asn Val Asp Ser Asp Tyr  
   1                  5                  10                  15

gct ctc gat ctg ctt gaa cgg ctt gat tcc aac tgg aag ggc acc gag 96  
 Ala Leu Asp Leu Leu Glu Arg Leu Asp Ser Asn Trp Lys Gly Thr Glu  
                   20                  25                  30

ctc ttt act cat ata cgc gaa acc ttt caa att ggc ctt ggc aat gtt 144  
 Leu Phe Thr His Ile Arg Glu Thr Phe Gln Ile Gly Leu Gly Asn Val  
                   35                  40                  45

atc ata gtg tca gaa cag agt gaa agc ctt aga ata ccc cct tca cta 192

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Ile	Ile	Val	Ser	Glu	Gln	Ser	Glu	Ser	Leu	Arg	Ile	Pro	Pro	Ser	Leu		
	50					55					60						
ctt	ggt	agc	agt	agt	cca	gca	gat	agc	gac	aat	agt	cct	cca	gga	aca	240	
Leu	Gly	Ser	Ser	Ser	Pro	Ala	Asp	Ser	Asp	Asn	Ser	Pro	Pro	Gly	Thr	80	
65					70					75							
cct	act	aat	gaa	gcg	caa	ccc	tgg	ttt	att	tct	gaa	gat	ctc	tcg	aaa	288	
Pro	Thr	Asn	Glu	Ala	Gln	Pro	Trp	Phe	Ile	Ser	Glu	Asp	Leu	Ser	Lys	95	
			85					90									
ggc	cct	ttc	acg	gaa	gcc	cag	tca	act	caa	tca	tct	att	gag	aca	ctc	336	
Gly	Pro	Phe	Thr	Glu	Ala	Gln	Ser	Thr	Gln	Ser	Ser	Ile	Glu	Thr	Leu	110	
			100					105									
gaa	ggt	gag	cac	cat	gct	gtg	tct	tct	ctg	cac	ctg	aag	cta	aat	ggc	384	
Glu	Gly	Glu	His	His	Ala	Val	Ser	Ser	Leu	His	Leu	Lys	Leu	Asn	Gly	125	
			115				120										
ctc	tcc	tgt	att	gga	cgt	gct	gta	tgg	cgg	gct	act	cgc	aaa	atg	gat	432	
Leu	Ser	Cys	Ile	Gly	Arg	Ala	Val	Trp	Arg	Ala	Thr	Arg	Lys	Met	Asp	140	
			130				135										
acg	aga	aca	gag	gtg	gac	gac	ata	tta	aac	tca	ata	aca	gaa	ccc	aga	480	
Thr	Arg	Thr	Glu	Val	Asp	Asp	Ile	Leu	Asn	Ser	Ile	Thr	Glu	Pro	Arg	160	
					150					155							
aga	ctc	aca	tta	ccc	ggt	atc	aac	aag	atg	cgt	caa	tgc	att	gtg	cgt	528	
Arg	Leu	Thr	Leu	Pro	Gly	Ile	Asn	Lys	Met	Arg	Gln	Cys	Ile	Val	Arg	175	
				165					170								
cta	ttg	ctt	ctc	gta	ccg	atc	caa	gta	cga	gaa	gag	atc	ctt	tct	ttc	576	
Leu	Leu	Leu	Leu	Val	Pro	Ile	Gln	Val	Arg	Glu	Glu	Ile	Leu	Ser	Phe	190	
			180					185									
gcc	ata	gct	tcg	ggg	ata	ccc	tca	gaa	aca	ata	gaa	gat	att	cga	tct	624	
Ala	Ile	Ala	Ser	Gly	Ile	Pro	Ser	Glu	Thr	Ile	Glu	Asp	Ile	Arg	Ser	205	
			195				200										
tca	aca	aat	att	tca	gct	gtt	gat	acc	aat	ggc	aga	ggc	ata	gca	cat	672	
Ser	Thr	Asn	Ile	Ser	Ala	Val	Asp	Thr	Asn	Gly	Arg	Gly	Ile	Ala	His	220	
			210			215											
aat	tcc	aaa	aag	cgg	tca	tta	gcg	cca	aca	caa	gat	tca	cgc	aat	tta	720	
Asn	Ser	Lys	Lys	Arg	Ser	Leu	Ala	Pro	Thr	Gln	Asp	Ser	Arg	Asn	Leu	240	
					230					235							
cgc	cgt	cga	atc	agg	gga	cat	acc	caa	tag							750	
Arg	Arg	Arg	Ile	Arg	Gly	His	Thr	Gln	*								
				245													

&lt;210&gt; 77

&lt;211&gt; 249

&lt;212&gt; PRT

&lt;213&gt; Zygosaccharomyces bailii

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&lt;400&gt; 77

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Met Asn Ser Glu Phe Ser Leu Ala Tyr Gly Asn Val Asp Ser Asp Tyr
 1          5          10          15
Ala Leu Asp Leu Leu Glu Arg Leu Asp Ser Asn Trp Lys Gly Thr Glu
 20          25          30
Leu Phe Thr His Ile Arg Glu Thr Phe Gln Ile Gly Leu Gly Asn Val
 35          40          45
Ile Ile Val Ser Glu Gln Ser Leu Arg Ile Pro Pro Ser Leu
 50          55          60
Leu Gly Ser Ser Ser Pro Ala Asp Ser Asp Asn Ser Pro Pro Gly Thr
 65          70          75          80
Pro Thr Asn Glu Ala Gln Pro Trp Phe Ile Ser Glu Asp Leu Ser Lys
 85          90          95
Gly Pro Phe Thr Glu Ala Gln Ser Thr Gln Ser Ser Ile Glu Thr Leu
100          105          110
Glu Gly Glu His His Ala Val Ser Leu His Leu Lys Leu Asn Gly
115          120          125
Leu Ser Cys Ile Gly Arg Ala Val Trp Arg Ala Thr Arg Lys Met Asp
130          135          140
Thr Arg Thr Glu Val Asp Asp Ile Leu Asn Ser Ile Thr Glu Pro Arg
145          150          155          160
Arg Leu Thr Leu Pro Gly Ile Asn Lys Met Arg Gln Cys Ile Val Arg
165          170          175
Leu Leu Leu Leu Val Pro Ile Gln Val Arg Glu Glu Ile Leu Ser Phe
180          185          190
Ala Ile Ala Ser Gly Ile Pro Ser Glu Thr Ile Glu Asp Ile Arg Ser
195          200          205
Ser Thr Asn Ile Ser Ala Val Asp Thr Asn Gly Arg Gly Ile Ala His
210          215          220
Asn Ser Lys Lys Arg Ser Leu Ala Pro Thr Gln Asp Ser Arg Asn Leu
225          230          235          240
Arg Arg Arg Ile Arg Gly His Thr Gln
245

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&lt;210&gt; 78

&lt;211&gt; 453

&lt;212&gt; DNA

<213> *Saccharomyces cerevisiae*

&lt;220&gt;

&lt;221&gt; promoter

&lt;222&gt; (1)...(450)

&lt;221&gt; misc\_feature

&lt;222&gt; (451)...(453)

&lt;223&gt; start codon

&lt;400&gt; 78

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ctacttattc ccttcgagat tataatctagg aacccatcag gttgggtggaa gattaccgct 60
tctaagactt ttcagcttcc tctattgatg ttacacctgg acaccccttt tctggcatcc 120
agtttttaat cttcagtggc atgtgagatt ctccgaaatt aattaaagca atcacacaat 180
tctctcggat accacctcgg ttgaaactga cagggtggtt gttacgcatg ctaatgcaaa 240
ggagcctata tacctttggc tcggctgctg taacagggaa tataaagggc agcataattt 300
aggagtttag tgaacttgca acatttacta ttttcccttc ttacgtaaat atttttcttt 360
ttaattctaa atcaatcttt ttcaattttt tgtttgtatt cttttcttgc ttaaattctat 420
aactacaaaa aacacatata taaactaaaa atg 453

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<210> 79  
 <211> 499  
 <212> DNA  
 <213> *Zygosaccharomyces bailii*

<220>  
 <221> promoter  
 <222> (1)...(496)

<221> misc\_feature  
 <222> (497)...(499)  
 <223> start codon

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 ggatcgtatt gcttccattc ttcttttgtt attcggcgcg attcgaattc atgacatctt 60  
 ttaaccgtcc gcactacatt actggctcaa gaaaggattg ataaatacta ccaaggaaca 120  
 cgtgtatcca ttgatactg tgctgggttac aagacacatg ctttacaagc acacttctat 180  
 ctctctcgac tgaggcgaaa cgtcgagtgg tttgatataca aatgcatgcg tgatatgcac 240  
 cattattttt ccccttttact tccgtcacgc cggggctcca cttttttggg ttccactttt 300  
 cttacgaccc tcgacatcca ctaaacgaac aggaagtcaa agaaccctc gagtcacacg 360  
 gtgcgtatgc gctgttaaca tatataaagg tcacctttcc ctgctcaaaa gagtcttagc 420  
 aggcgtgtaa cttcactctc tatcgatcca tagaatctaa ctaacaagag actacatcgg 480  
 tataacaaat aacaaaatg 499

<210> 80  
 <211> 27  
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 <213> Artificial Sequence

<220>  
 <223> PCR Primer

<400> 80  
 aagagactcc aacgtcgcgc acctgta 27

<210> 81  
 <211> 32  
 <212> DNA  
 <213> Artificial Sequence

<220>  
 <223> PCR Primer

<400> 81  
 agaggattag gaagacacaa attgcatggg ga 32

<210> 82  
 <211> 29  
 <212> DNA  
 <213> Artificial Sequence

<220>  
 <223> PCR Primer

<400> 82  
 atcgatttgc ttccattctt cttttgtta 29

<210> 83  
<211> 29  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> PCR Primer

<400> 83  
tttgttattt gttataaccga tgtagtctc 29

<210> 84  
<211> 27  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> PCR Primer

<400> 84  
tagctactct tctccaggtg tcattag 27

<210> 85  
<211> 25  
<212> DNA  
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<220>  
<223> PCR Primer

<400> 85  
cctatgtccg agtttagcga gcttg 25

<210> 86  
<211> 25  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> PCR Primer

<400> 86  
agaatgaact cagagttctc tcttg 25

<210> 87  
<211> 22  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> PCR Primer

<400> 87  
attctattgg gtatgtcccc tg 22

<210> 88  
<211> 30

&lt;212&gt; DNA

&lt;213&gt; Artificial Sequence

&lt;220&gt;

&lt;223&gt; PCR Primer

&lt;400&gt; 88

gtttttaatt ttgaagctca cctttaattg

30

&lt;210&gt; 89

&lt;211&gt; 26

&lt;212&gt; DNA

&lt;213&gt; Artificial Sequence

&lt;220&gt;

&lt;223&gt; PCR Primer

&lt;400&gt; 89

attatgttct ccagggaaga ggtag

26

&lt;210&gt; 90

&lt;211&gt; 27

&lt;212&gt; DNA

&lt;213&gt; Artificial Sequence

&lt;220&gt;

&lt;223&gt; PCR Primer

&lt;400&gt; 90

agaatcaatc atttagtgtg gcaggag

27

&lt;210&gt; 91

&lt;211&gt; 25

&lt;212&gt; DNA

&lt;213&gt; Artificial Sequence

&lt;220&gt;

&lt;223&gt; PCR Primer

&lt;400&gt; 91

taaaaaactgc ccgcatatt tcgtc

25

&lt;210&gt; 92

&lt;211&gt; 708

&lt;212&gt; DNA

&lt;213&gt; Zygosaccharomyces rouxii

&lt;400&gt; 92

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gtgcgcggcg	ctagcacgta	atgacccttg	atgacaaaact	ccaatggat	caccctactg	120
tcctctcccc	ctcccctttt	tttccttctt	tccttccatc	tatttctgat	ctcctcccct	180
cagcagatgt	cccgaaggt	acagctgcga	tacgggcagc	cactttttga	cgtctcgcaa	240
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gccgccgagg	gtgggggtata	aagggctaca	tccttacccc	cacgcaggcg	ataacccgca	360
tcatacaact	gtcctcctct	tccgctctcg	ccactagccg	ccgaaccatt	gctaccgcaa	420
tgacaccgtg	tggatgatctc	aagggaggat	gtgtgggtgt	gggacggaac	ttccactttt	480
tcctcagtag	gtgcgatgcc	ccctacaccg	agcttcact	aacgtgtttc	agcggttgaa	540

ggcaatggga tcgcagaatt atcgagcgtt gttggtatat aaagggagaa gatatatgga 600  
taagagacat gttctacttc tggtctctct ttctttttat cctatatcac cagaacaaat 660  
caagttcgca ttgattcata tcaaataaaa agtacatcac agataaca 708

<210> 93

<211> 21

<212> DNA

<213> Artificial Sequence

<220>

<223> PCR Primer

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<210> 94

<211> 29

<212> DNA

<213> Artificial Sequence

<220>

<223> PCR Primer

<400> 94

tgtctgtgat gtacttttta tttgatatg 29

<210> 95

<211> 25

<212> DNA

<213> Artificial Sequence

<220>

<223> PCR Primer

<400> 95

acgcaagaga gaactctgag ttcac 25